



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 111937

TO: Jeanine Goldberg

Location: cm1/12d11

Art Unit: 1634

Tuesday, January 13, 2004

Case Serial Number: 10/035978

From: Barb O'Bryen

Location: Biotech-Chem Library

CM1-6A05

Phone: 308-4291

*BOB*  
barbara.obryen@uspto.gov

### Search Notes

Jeanine,

Seq 126 is 105nt long, so I didn't use the suggested length limitation for the Registry search  
(there were only 6 hits).

Barb

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

DB nucleic - nucleic search, using sw model  
 run on: January 12, 2004, 22:35:58 ; Search time 2659 Seconds  
 (without alignments)  
 1615.461 Million cell updates/sec

Title: US-10-035-978a-126

perfect score: 105

sequence: 1 ccctttagtttcctcgctt.....attccagccatgtgggg 105

scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_on:\*

5: gb\_ov:\*

6: gb\_dat:\*

7: gb\_bh:\*

8: gb\_D1:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_v1:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_dat:\*

24: em\_ph:\*

25: em\_D1:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_v1:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_D1:\*

35: em\_htg\_rod:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

	Result No.	Score	Query	Match Length	DB ID	Description
	1	105	100.0	105	1	HPY390718
	2	105	100.0	105	1	HPY390719
	3	105	100.0	105	6	BD009534
	4	105	100.0	105	6	BD009535
	5	105	100.0	223	1	AB057126
	6	103.4	98.5	105	1	AB057120
	7	103.4	98.5	105	6	BD009536
	8	101.8	97.0	105	1	HPY390721
	9	101.8	97.0	105	6	BD009540
	10	101.8	97.0	223	1	AB057113
	11	101.8	97.0	223	1	AB057141
	12	101.8	97.0	223	1	AB057158
	13	101.8	97.0	256	1	AF050377
	14	101.8	97.0	631	1	AF091830
	15	100.2	95.4	105	1	HPY390723
	16	100.2	95.4	105	1	HPY390724
	17	100.2	95.4	105	1	HPY390726
	18	100.2	95.4	105	6	BD009537
	19	100.2	95.4	105	6	BD009539
	20	100.2	95.4	105	6	BD009541
	21	100.2	95.4	223	1	AB057114
	22	100.2	95.4	223	1	AB057118
	23	100.2	95.4	223	1	AB057119
	24	100.2	95.4	223	1	AB057132
	25	100.2	95.4	223	1	AB057137
	26	100.2	95.4	223	1	AB057148
	27	100.2	95.4	223	1	AB057153
	28	100.2	95.4	223	1	AB057159
	29	100.2	95.4	223	1	AB057162
	30	100.2	95.4	223	1	AB057165
	31	100.2	95.4	631	1	AF091829
	32	100.2	95.4	631	1	AF091833
	33	100.2	95.4	4195	1	AF049629
	34	100.2	95.4	4196	1	AF049640
	35	100.2	95.4	4207	1	AF049331
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	40	98.8	94.1	251	1	AP035614
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	43	98.6	93.9	105	6	BD009545
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## ALIGNMENTS

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KEYWORDS		SOURCE		Vaca Gene; Vaca Protein.
ORGANISM				Helicobacter pylori
				Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
REFERENCE	1	AUTHORS	van Doorn,L.J., Figueiredo,C., Sianna,R., Pena,S., Midolo,P., Ng,E.K., Atierton,J.C., Blaser,M.J. and Quint,W.G.	

Pred. No. is the number of results predicted by chance to have a

Ng, E.K., Atierton, J.C., Blaser, M.J. and Quint, W.G.





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 1 (bases 1 to 105)  
 Quint,W. and Doorn,L.J.V.  
 Probes, methods and kits for detection and typing of Helicobacter  
 pylori nucleic acids in biological samples.  
 Patent: JP 200150536-A 128 27-PBB-2001;  
 INNOGENETICS NV, Dri, BV  
 OS Unidentified  
 COMMENT PN JP 200152536-A/128  
 PD 27-PBB-2001  
 PF 10-PBB-1997 JP 1998518004  
 PR 16-OCT-1997 EP 9687031.8  
 PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN  
 PC C1201/68, C07K14/205, C12N15/11  
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 VERSION 1  
 KEYWORDS vacA gene; VacA protein.  
 SOURCE  
 ORGANISM Helicobacter pylori  
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacter; Helicobacter.  
 REFERENCE 1  
 AUTHORS van Doorn,L.J., Figueiredo,C., Sanna,R., Pena,S., Midolo,O., P., Ng,E.K., Atherton,J.C., Blaser,M.J. and Quint,W.G.  
 TITLE Expanding allelic diversity of Helicobacter pylori vacA  
 JOURNAL J.Clin.Microbiol. 36 (9), 2597-2603 (1998)  
 PUBMED 98371099  
 REFERENCE 2 (bases 1 to 105)  
 AUTHORS van Doorn,L.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-OCT-1999) van Doorn,L.J., Molecular Biology, Delft Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD, NETHERLANDS  
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 SOURCE JP\_200102536\_A/132.  
 ORGANISM unidentified  
 unclassified  
 1 (bases 1 to 105)  
 Quint, W. and Doorn,L.J.V.  
 Authors Probe, methods and kits for detection and typing of Helicobacter  
 pylori nucleic acids in biological samples  
 TITLE Patent: JP 200102536-A 132 27-FEB-2001;  
 INNOGENETICS NV, DDL BV  
 Unidentified  
 OS Unidentified  
 PN JP 2001502536-A/132  
 PD 27-FEB-2001  
 PP 10-OCT-1997 JP 1998518004  
 PR 16-OCT-1996 EP 96870131-8  
 PI WILHELMUS QUINT/LEENDERT JAN VAN DOORN  
 PC C12Q1/68, C07K14/205, C12N1/11  
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 LOCUS 223 bp DNA linear BCT 02-APR-2002  
 DEFINITION Helicobacter pylori vaca gene for vacuolating cytotoxin, partial  
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 ACCESSION AB057141  
 VERSION AB057141.1  
 GI:19910513  
 KEYWORDS SOURCE  
 ORGANISM Helicobacter pylori  
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 Helicobacteraceae; Helicobacter.  
 REFERENCE 1  
 AUTHORS Yamaoka, Y., Gutierrez, O., Saitou,N., Kodama,T., Kim,J.G.,  
 Kashima, K., Ramirez,P.C., Mahachai,V., Osato,M.S. and Graham,D.Y.  
 TITLE Direct Submission  
 JOURNAL Studies of human migration  
 PUBLISHED Unpublished (bases 1 to 223)  
 AUTHORS Yamaoka, Y., Gutierrez, O., Saitou,N., Kodama,T., Kim,J.G.,  
 Kashima, K., Ramirez,P.C., Mahachai,V., Osato,M.S. and Graham,D.Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAR-2001) Yoshiro Yamada, Baylor College of Medicine,  
 Department of Medicine, VA Medical Center (111D),  
 Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net),  
 Tel:713-790-7234, Fax:713-790-1040)  
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 ORGANISM unidentified  
 unclassified  
 1 (bases 1 to 223)  
 Quint, W. and Doorn,L.J.V.  
 Authors Probe, methods and kits for detection and typing of Helicobacter  
 pylori nucleic acids in biological samples  
 TITLE Patent: JP 200102536-A 132 27-FEB-2001;  
 INNOGENETICS NV, DDL BV  
 Unidentified  
 OS Unidentified  
 PN JP 2001502536-A/132  
 PD 27-FEB-2001  
 PP 10-OCT-1997 JP 1998518004  
 PR 16-OCT-1996 EP 96870131-8  
 PI WILHELMUS QUINT/LEENDERT JAN VAN DOORN  
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 RESULT 11 AB057141  
 LOCUS 223 bp DNA linear BCT 02-APR-2002  
 DEFINITION Helicobacter pylori vaca gene for vacuolating cytotoxin, partial  
 cds, signal sequence, strain:JapanK26.  
 ACCESSION AB057141  
 VERSION AB057141.1  
 GI:19910513  
 KEYWORDS SOURCE  
 ORGANISM Helicobacter pylori  
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 Helicobacteraceae; Helicobacter.  
 REFERENCE 1  
 AUTHORS Yamaoka, Y., Gutierrez, O., Saitou,N., Kodama,T., Kim,J.G.,  
 Kashima, K., Ramirez,P.C., Mahachai,V., Osato,M.S. and Graham,D.Y.  
 TITLE Direct Submission  
 JOURNAL Studies of human migration  
 PUBLISHED Unpublished (bases 1 to 223)  
 AUTHORS Yamaoka, Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G.,  
 Kashima, K., Ramirez,P.C., Mahachai,V., Osato,M.S. and Graham,D.Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAR-2001) Yoshiro Yamada, Baylor College of Medicine,  
 Department of Medicine, VA Medical Center (111D),  
 Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net),  
 Tel:713-790-7234, Fax:713-790-1040)  
 FEATURES Location/Qualifiers  
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XX WPI; 1998-251300/22.  
 XX Method for detecting and/or typing Helicobacter pylori strains -  
 PT comprises use of primers and probes based on vacA and caga gene  
 XX  
 PS C'aim 19; Figure 12; 122pp; English.  
 XX  
 CC This invention describes a novel method for the detection and/or typing  
 CC of Helicobacter pylori strains present in a sample using PCR primers and  
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other  
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)  
 CC gene. The method allows the typing and allele-specific detection of a  
 CC strain according to the VDG alleles present in that particular H. pylori  
 CC strain. The virulence determinant genes are the genetic elements  
 CC involved in enabling, determining, and marking the infectivity and/or  
 CC pathogenicity of the H. pylori strain. The method provides a way of  
 CC detecting H. pylori strains in a sample with respect to the development  
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric  
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or  
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers  
 CC and probes used in the detection of the H. pylori vacA and caga genes.  
 CC The primers and probes are used especially to detect the vacA S regions  
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in  
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 XX DT 22-MAR-2000 (first entry)  
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 XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;  
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;  
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;  
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;  
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.  
 XX OS Helicobacter pylori.  
 XX PN WO9816658-A2.  
 XX PR 16-OCT-1996; 96EP-0870131.  
 PD 23-APR-1998.  
 XX PR 09-SEP-1997; 97EP-0870133.  
 XX PR 10-OCT-1997; 97WO-EP05614.  
 XX PA (INNO-) INNOGENETICS NV.  
 PA (DDLD-) DDL BV.  
 XX PI Quint W, Van Doorn L;  
 XX DR WPI; 1998-251300/22.

DR WPI; 1998-251300/22.  
 XX Method for detecting and/or typing Helicobacter pylori strains -  
 PT comprises use of primers and probes based on vacA and caga gene  
 XX  
 PS Claim 19; Figure 12; 122pp; English.  
 XX  
 CC This invention describes a novel method for the detection and/or typing  
 CC of Helicobacter pylori strains present in a sample using PCR primers and  
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other  
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)  
 CC gene. The method allows the typing and allele-specific detection of a  
 CC strain according to the VDG alleles present in that particular H. pylori  
 CC strain. The virulence determinant genes are the genetic elements  
 CC involved in enabling, determining, and marking the infectivity and/or  
 CC pathogenicity of the H. pylori strain. The method provides a way of  
 CC detecting H. pylori strains in a sample with respect to the development  
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric  
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or  
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers  
 CC and probes used in the detection of the H. pylori vacA and caga genes.  
 CC The primers and probes are used especially to detect the vacA S regions  
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in  
 CC AAV73547-V73785.  
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 XX DT 22-MAR-2000 (first entry)  
 DE H. pylori vacA S-region s1c DNA Fragment HK51001.  
 XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;  
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;  
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;  
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;  
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.  
 XX OS Helicobacter pylori.  
 XX PN WO9816658-A2.  
 XX PR 16-OCT-1996; 96EP-0870131.  
 PD 23-APR-1998.  
 XX PR 09-SEP-1997; 97EP-0870133.  
 XX PR 10-OCT-1997; 97WO-EP05614.  
 XX PA (INNO-) INNOGENETICS NV.  
 PA (DDLD-) DDL BV.  
 XX PI Quint W, Van Doorn L;  
 XX DR WPI; 1998-251300/22.



PT comprises use of primers and probes based on vcaA and caga gene  
 XX Claim 13; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing  
 CC of Helicobacter pylori strains present in a sample using PCR primers and  
 CC probes to detect regions of the vacuolating toxin (vaca) gene and other  
 CC virulence determinant genes (VDG), e.g. the cytotoxin-associated (caga)  
 CC gene. The method allows the typing and allele-specific detection of a  
 CC strain according to the VDG alleles present in that particular H. pylori  
 CC strain. The virulence determinant genes are the genetic elements  
 CC involved in enabling, determining, and marking the infectivity and/or  
 CC pathogenicity of the H. pylori strain. The method provides a way of  
 CC detecting H. pylori strains in a sample with respect to the development  
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric  
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or  
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers  
 CC and probes used in the detection of the H. pylori vcaA and caga genes.  
 CC The primers and probes are used especially to detect the vcaA S regions  
 CC S1a/b/C and S2 and the M regions M1 and M2 which are represented in  
 CC AAV73547-V73785.  
 XX Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;  
 SQ

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps	Other
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 AC AAV73639;  
 XX DT 22-MAR-2000 (first entry)

DB H. pylori vcaA S-region SIC DNA fragment 95\_24001.  
 XX PCR primer; probe; vcaA; caga; detection; vacuolating toxin; VDG;  
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;  
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;  
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;  
 KW S region; S1a; S1b; S2; M region; M1; M2; 88.  
 XX OS Helicobacter pylori.  
 PN WO9816658-A2.  
 XX PD 23-APR-1998.  
 XX PP 10-OCT-1997; 97WO-EP05614.

XX PR 16-OCT-1996; 96EP-0870131.  
 PR 09-SEP-1997; 97EP-0870133.  
 XX PA (INNO-) INNOGENETICS NV.  
 PA (DDLD-) DDL BY.  
 XX PI Quint W, Van Doorn L;  
 XX DR WPI; 1998-251300/22.  
 XX PT Method for detecting and/or typing Helicobacter pylori strains -  
 PT comprises use of primers and probes based on vcaA and caga gene

XX Claim 19; Figure 12; 122pp; English.  
 XX This invention describes a novel method for the detection and/or typing  
 CC of Helicobacter pylori strains present in a sample using PCR primers and  
 CC probes to detect regions of the vacuolating toxin (vaca) gene and other  
 CC virulence determinant genes (VDG), e.g. the cytotoxin-associated (caga)  
 CC gene. The method allows the typing and allele-specific detection of a  
 CC strain. The virulence determinant genes are the genetic elements  
 CC involved in enabling, determining, and marking the infectivity and/or  
 CC pathogenicity of the H. pylori strain. The method provides a way of  
 CC detecting H. pylori strains in a sample with respect to the development  
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric  
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or  
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers  
 CC and probes used in the detection of the H. pylori vcaA and caga genes.  
 CC The primers and probes are used especially to detect the vcaA S regions  
 CC S1a/b/C and S2 and the M regions M1 and M2 which are represented in  
 CC AAV73547-V73785.  
 XX Sequence 105 BP; 20 A; 28 C; 24 G; 33 T; 0 other;  
 SQ

Query	Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps	Other
QY	1 CCCTTAGTTCTCGCTTAGGGGTATGGTCAGCATCACACAAAAAGTC	95.4%	105;	97.1%	1.6e-23;	0;	0;	0;	0;
Db	1 CCCTTAGTTCTCGCTTAGGGGTATGGTCAGCATCACACAAAAAGTC								
QY	61 TGCTGCCCTCTTACACGGTATCCAGGCATTGTTGGGG	105							
Db	61 TGCGCCCTCTTACACGGTATCCAGGCATTGTTGGGG	105							

RESULT 7  
 ID AAV73641 standard; DNA; 105 BP.  
 XX  
 AC AAV73641;  
 XX DT 22-MAR-2000 (first entry)

DB H. pylori vcaA S-region SIC DNA fragment TH8828001.  
 XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;  
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;  
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;  
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;  
 KW S region; S1a; S1b; S2; M region; M1; M2; 88.  
 XX OS Helicobacter pylori.  
 PN WO9816658-A2.  
 XX PD 23-APR-1998.  
 XX PP 10-OCT-1997; 97WO-EP05614.  
 XX PR 16-OCT-1996; 96EP-0870131.  
 PR 09-SEP-1997; 97EP-0870133.  
 XX PA (INNO-) INNOGENETICS NV.  
 PA (DDLD-) DDL BY.  
 XX PI Quint W, Van Doorn L;  
 XX DR WPI; 1998-251300/22.  
 XX PT Method for detecting and/or typing Helicobacter pylori strains -  
 PT comprises use of primers and probes based on vcaA and caga gene



This invention describes a novel method for the detection and/or typing of Helicobacter pylori strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vacA) gene and other virulence determinant genes (VDG), e.g., the cytotoxin-associated (caga) gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular H. pylori strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the H. pylori vacA and caga genes. The primers and probes are used especially to detect the vacA S regions S1a/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

**Sequence 105 BP; 23 A; 28 C; 21 G; 33 T; 0 other;**

Query Match	93.9%;	Score	98.6;	DB	19;	Length	105;
Best Local Similarity	96.2%;	Pred. No.	5.3e-23;				
Matches	101;	Conservative	0;	Mismatches	4;	Indels	0;
Gaps	0;						

QY      1 CCCCCTTAGTTCTCCTCGGTTACTGGGGTATGGTCGATCACACCAAAAAACTCA 60  
DB      1 CCCCCTTAGTTCTCCTCGGTTACTGGGGTATGGTCGATCACACCAAAAAACTCA 60

QY      61 TGCTGCCTTACACCGTGATCATCCAGGCAATTGGGG 105  
DB      61 TGCCGCCCTTTTACACCGTGATCATCCAGGCAATTGGGG 105

**RESULT 10**

AAV73645  
ID AAV73645 standard; DNA; 105 BP.  
XX  
AC  
AAV73645;  
XX

DT 22-MAR-2000 (first entry)  
XX  
H. pylori vacA S-region SIC DNA fragment TH8832001.

XX  
PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG; virulence determinant gene; cytotoxin-associated gene; allele-specific; infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer; adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy; S region; Sia; Sib; Sic; S2; M region; M1; M2; ss.  
OS  
Helicobacter pylori.  
XX  
W09816658-A2.

XX  
23-APR-1998.  
PD  
XX  
PP  
10-OCT-1997;  
XX  
97WO-EP05614.  
PR  
16-OCT-1996;  
PR  
09-SEP-1997;  
XX  
96EP-0870131.  
97EP-0870133.  
PA  
(INNO-) INNOGENETICS NV.  
PA  
(DDLD-) DDL BV.  
XX  
PI  
Quint W, Van Doorn L;  
XX  
DR  
WPI, 1998-251300/22.

XX  
Method for detecting and/or typing Helicobacter pylori strains -  
PR comprises use of primers and probes based on vacA and caga gene  
PS  
Claim 19; Figure 12; 122pp; English.  
XX  
This invention describes a novel method for the detection and/or typing  
CC  
of Helicobacter pylori strains present in a sample using PCR primers and

CC of Helicobacter pylori strains present in a sample using PCR primers and  
CC probes to detect regions of the vacuolating toxin (vacA) gene and other  
CC virulence determinant genes (VDG), e.g., the cytotoxin-associated (caga)  
CC gene. The method allows the typing and allele-specific detection of a  
CC strain according to the VDG alleles present in that particular H. pylori  
CC strain. The virulence determinant genes are the genetic elements  
CC involved in enabling, determining, and marking the infectivity and/or  
CC pathogenicity of the H. pylori strain. The method provides a way of  
CC detecting H. pylori strains in a sample with respect to the development  
CC of chronic active gastritis, gastric and duodenal ulcers, gastric  
CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or  
CC determining eradication therapy. AAV73508-V73546 represent PCR primers  
CC and probes used in the detection of the H. pylori vacA and caga genes.  
CC The primers and probes are used especially to detect the vacA S regions  
CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in  
CC AAV73547-V73785.

XX  
Sequence 105 BP; 23 A; 28 C; 21 G; 33 T; 0 other;

Query	Match	93.9%;	Score	98.6;	DB	19;	Length	105;
Best Local Similarity	96.2%;	Pred. No.	5.3e-23;					
Matches	101;	Conservative	0;	Mismatches	4;	Indels	0;	
Gaps	0;							

QY      1 CCCTTTAGTTCTCCTCGGTTACTGGGGTATGGTCGATCACACCAAAAAACTCA 60  
DB      1 CCCTTTAGTTCTCCTCGGTTACTGGGGTATGGTCGATCACACCAAAAAACTCA 60

QY      61 TGCTGCCTTACACCGTGATCATCCAGGCAATTGGGG 105  
DB      61 TGCCGCCCTTTTACACCGTGATCATCCAGGCAATTGGGG 105

**RESULT 11**

AAV73550  
ID AAV73550 standard; DNA; 176 BP.  
XX  
AC  
AAV73550;  
XX

DT 22-MAR-2000 (first entry)  
XX  
H. pylori S-region S1a/b fragment C4082\_VA1F.

XX  
DE  
XX  
PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;  
KW  
virulence determinant gene; cytotoxin-associated gene; allele-specific;  
KW  
infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;  
KW  
adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;  
KW  
S region; Sia; Sib; Sic; S2; M region; M1; M2; ss.  
XX  
Helicobacter pylori.  
OS  
PN  
W09816658-A2.  
XX  
23-APR-1998.  
PD  
XX  
PP  
10-OCT-1997;  
XX  
97WO-EP05614.  
PR  
16-OCT-1996;  
PR  
09-SEP-1997;  
XX  
96EP-0870131.  
97EP-0870133.  
PA  
(INNO-) INNOGENETICS NV.  
PA  
(DDLD-) DDL BV.  
XX  
PI  
Quint W, Van Doorn L;  
XX  
DR  
WPI, 1998-251300/22.

XX  
Method for detecting and/or typing Helicobacter pylori strains -  
PR comprises use of primers and probes based on vacA and caga gene  
PS  
Claim 17; Figure 2a; 122pp; English.  
XX  
This invention describes a novel method for the detection and/or typing  
CC  
of Helicobacter pylori strains present in a sample using PCR primers and

probes to detect regions of the vacuolating toxin (vacA) gene and other virulence determinant genes (VDG), e.g. the cytotoxin-associated (caga) gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular H. pylori strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphomas, and/or determining eradication therapy. AAV73547-V73546 represent PCR primers and probes used in the detection of the H. pylori vacA and caga genes. The primers and probes are used especially to detect the vacA S regions S1a/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

XX Sequence 176 BP; 39 A; 43 C; 45 G; 49 T; 0 other;

XX Query Match 93.9%; Score 98.6; DB 19; Length 176;

XX Best Local Similarity 96.2%; Pred. No. 6.1e-23;

XX Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTCTCGCTTGTAGGGTTATTGGTCAGCATCACCCACAAAAAAAGTCA 60

Db 2 CCCTTAGTTCTCGCTTGTAGGGTTATTGGTCAGCATCACCCACAAAAAAAGTCA 61

Dy 61 TGCTGCCTCTTACACCGTGATCATTCAGGCCATTGGGG 105

Db 62 TGCGGCCTTTACACCGTGATCATTCAGGCCATTGGGG 106

<RESULT 12  
AAV73650

ID AAV73650 standard; DNA; 105 BP.

XX

AAV73650;

XX

22-MAR-2000 (first entry)

XX

H. pylori vacA S-region sIC DNA fragment CH4001.

XX

PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;

XX virulence determinant gene; cytotoxin-associated gene; allele-specific;

XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;

XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;

XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX

Helicobacter pylori.

XX

WO9816658-A2.

XX

23-APR-1998.

XX

10-OCT-1997; 97WO-EP05614.

XX

16-OCT-1996; 96EP-0870131.

XX

09-SEP-1997; 97EP-0870133.

XX

(INNO-) INNOGENETICS NV.

(DDLD-) DDL BV.

XX

Quint W, Van Doorn L;

XX

DR, 1998-251300/22.

XX

Method for detecting and/or typing Helicobacter pylori strains -

XX comprises use of primers and probes based on vacA and caga gene

XX

PS Claim 19; Figure 12; 122PP; English.

XX

This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and

CC probes to detect regions of the vacuolating toxin (vacA) gene and other

CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)

CC gene. The method allows the typing and allele-specific detection of a

CC strain according to the VDG alleles present in that particular H. pylori

CC strain. The virulence determinant genes are the genetic elements

CC involved in enabling, determining, and marking the infectivity and/or

CC pathogenicity of the H. pylori strain. The method provides a way of

CC detecting H. pylori strains in a sample with respect to the development

CC of chronic active gastritis, gastric and duodenal ulcers, gastric

CC adenocarcinomas, mucosa-associated lymphomas, and/or

CC determining eradication therapy. AAV73508-V73546 represent PCR primers

CC and probes used in the detection of the H. pylori vacA and caga genes.

CC The primers and probes are used especially to detect the vacA S regions

CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in

CC AAV73547-V73785.

XX Sequence 105 BP; 21 A; 29 C; 31 T; 1 other;

XX SQ Query Match 93.1%; Score 97.8; DB 19; Length 105;

XX Best Local Similarity 95.2%; Pred. No. 9.8e-23;

XX Matches 100; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTCTCGCTTGTAGGGTTATTGGTCAGCATCACCCACAAAAAAAGTCA 60

Db 1 CCCTTAGTTCTCGCTTGTAGGGTTATTGGTCAGCATCACCCACAAAAAAAGTCA 60

Qy 61 TCTCTCTTCTTACACCGTGATCATTCAGGCCATTGGGG 105

Db 61 TGCCGCCTCTTTACACCGTGATCATTCAGGCCATTGGGG 105

RESULT 13

AAV73642

ID AAV73642 standard; DNA; 105 BP.

XX

AAV73642;

XX

DT 22-MAR-2000 (first entry)

XX

H. pylori vacA S-region sIC DNA fragment 95\_20001.

XX

PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;

XX virulence determinant gene; cytotoxin-associated gene; allele-specific;

XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;

XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;

XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX

Helicobacter pylori.

XX

W09816658-A2.

XX

23-APR-1998.

XX

PD 10-OCT-1997; 97WO-EP05614.

XX

PR 16-OCT-1996; 96EP-0870131.

XX

09-SEP-1997; 97EP-0870133.

XX

(INNO-) INNOGENETICS NV.

(DDLD-) DDL BV.

XX

PI Quint W, Van Doorn L;

XX

DR, 1998-251300/22.

XX

Method for detecting and/or typing Helicobacter pylori strains -

XX comprises use of primers and probes based on vacA and caga gene

XX

PS Claim 19; Figure 12; 122PP; English.

XX

This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and

CC probes to detect regions of the vacuolating toxin (vacA) gene and other

CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)

CC gene. The method allows the typing and allele-specific detection of a

CC strain according to the VDG alleles present in that particular H. pylori

CC strain. The virulence determinant genes are the genetic elements

CC involved in enabling, determining, and marking the infectivity and/or

CC pathogenicity of the H. pylori strain. The method provides a way of

CC detecting H. pylori strains in a sample with respect to the development

CC of chronic active gastritis, gastric and duodenal ulcers, gastric

CC adenocarcinomas, mucosa-associated lymphomas, and/or

CC determining eradication therapy. AAV73508-V73546 represent PCR primers

CC and probes used in the detection of the H. pylori vacA and caga genes.

CC The primers and probes are used especially to detect the vacA S regions

CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in

CC AAV73547-V73785.

XX This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and

CC probes to detect regions of the vacuolating toxin (vacA) gene and other

CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)

CC gene. The method allows the typing and allele-specific detection of a

CC strain according to the VDG alleles present in that particular H. pylori

CC strain. The virulence determinant genes are the genetic elements

CC involved in enabling, determining, and marking the infectivity and/or

CC pathogenicity of the H. pylori strain. The method provides a way of

CC detecting H. pylori strains in a sample with respect to the development

CC of chronic active gastritis, gastric and duodenal ulcers, gastric

CC adenocarcinomas, mucosa-associated lymphomas, and/or

CC determining eradication therapy. AAV73508-V73546 represent PCR primers

CC and probes used in the detection of the H. pylori vacA and caga genes.

CC The primers and probes are used especially to detect the vacA S regions

CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in

CC AAV73547-V73785.

XX This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and

CC probes to detect regions of the vacuolating toxin (vacA) gene and other

CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)

CC gene. The method allows the typing and allele-specific detection of a

CC strain according to the VDG alleles present in that particular H. pylori

CC strain. The virulence determinant genes are the genetic elements

CC involved in enabling, determining, and marking the infectivity and/or

CC pathogenicity of the H. pylori strain. The method provides a way of

CC detecting H. pylori strains in a sample with respect to the development

CC of chronic active gastritis, gastric and duodenal ulcers, gastric

CC adenocarcinomas, mucosa-associated lymphomas, and/or

CC determining eradication therapy. AAV73508-V73546 represent PCR primers

CC and probes used in the detection of the H. pylori vacA and caga genes.

CC The primers and probes are used especially to detect the vacA S regions

CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in

CC AAV73547-V73785.

CC gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular H. pylori strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the H. pylori vacA and cagA genes. The primers and probes are used especially to detect the vacA S regions S1a/b/C and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

XX Sequence 105 BP; 20 A; 28 C; 24 G; 33 T; 0 other;

Query	Match	Score	DB	Length
Qy	1 CCCCTTACGTTCTCGCTTTCAGCTGGCTTATGGTAGCATCACACACAAAAAAAGTCA	97	19	105
Db	1 CCCCTTACGTTCTCGCTTTCAGCTGGCTTATGGTAGCATCACACGGCAAAAGTCA	95.2	22	105
Qy	61 TGCTGCCTCTTACAACCGTGTATGCCAGCATGGTGGGG 105	95	19	105
Db	61 TGCGCCTTTACAACCGTGTATGCCAGCATGGTGGGG 105	95	19	105

RESULT 14

ID	AAV73649	Standard	DNA	105 BP.
----	----------	----------	-----	---------

XX AAV73649;

XX AC AAV73649;

XX DT 22-MAR-2000 (first entry)

DS H. pylori vacA S-region s1c DNA fragment NIP2001.

XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG; virulence determinant gene; cytotoxin-associated gene; allele-specific; infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer; adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy; S region; sia; sib; sic; S2; M region; M1; M2; ss.

OS Helicobacter pylori.

XX WO9816658-A2.

XX PN

XX PD 23-APR-1998.

XX PR 10-OCT-1997;

XX 97WO-EP05614.

XX 16-OCT-1996;

PR 09-SEP-1997;

XX 96EP-0870131;

DR 97EP-0870133.

XX PA (INNO-) INNOGENETICS NV.

PA (DDID-) DDL BV.

XX PI Quint W, Van Doorn L;

XX DR WPI; 1998-251300/22.

XX PT Method for detecting and/or typing Helicobacter pylori strains -

PT comprises use of primers and probes based on vacA and caga gene

XX PS Claim 19; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and

CC probes to detect regions of the vacuolating toxin (vacA) gene and other

CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)

CC gene. The method allows the typing and allele-specific detection of a

CC strain according to the VDG alleles present in that particular H. pylori

CC strain.

CC

</

strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the H. pylori strain. The method provides a way of detecting H. pylori strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the H. pylori vacA and cagA genes. The primers and probes are used especially to detect the vacA S regions S1a/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

IQ Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;

Query Match 92.4%; Score 97; DB 19; Length 105;

Best Local Similarity 95.2%; Pred. No. 1.8e-22;  
Matches 100; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Y 1 CCCTTAGTTCTCGGTTAGGGTTATGGTCAACCAAAAGTCA 60  
1 CCCCTGGTTCTCGGTTATGGTCAACCAAAAGTCA 60

b 1 CCCCTGGTTCTCGGTTATGGTCAACCAAAAGTCA 60

Y 61 TGCCTGCTTCCTAACACCGTGATCATTCAGCATTGGGG 105

b 61 TGCCTGCTTCCTAACACCGTGATCATTCAGCATTGGGG 105

Search completed: January 13, 2004, 01:27:30  
of time : 277 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 01:07:41 ; Search time 61 Seconds  
(without alignments)  
759.758 Million cell updates/sec

Title: US-10-035-978A-126

Perfect score: 105

Sequence: 1 cccctttagtttcctcgct.....attccaggccatgttgggg 105

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/podata/2/ina/5A\_COMB.seq:\*

2: /cgn2\_6/podata/2/ina/5B\_COMB.seq:\*

3: /cgn2\_6/podata/2/ina/6A\_COMB.seq:\*

4: /cgn2\_6/podata/2/ina/6B\_COMB.seq:\*

5: /cgn2\_6/podata/2/ina/pectus\_COMB.seq:\*

6: /cgn2\_6/podata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87.4	83.2	4042	1 US-08-200-232-1	Sequence 1, Appli
2	87.4	83.2	4042	5 PCT-US95-02219A-1	Sequence 1, Appli
3	87.4	83.2	4042	5 PCT-US95-02219A-1	Sequence 1, Appli
4	85.8	81.7	3960	3 US-08-470-260-2	Sequence 2, Appli
5	85.8	81.7	3960	3 US-08-471-491-2	Sequence 2, Appli
6	85.8	81.7	3960	3 US-08-466-662-2	Sequence 2, Appli
7	39.4	37.5	1419	2 US-08-295-643-1	Sequence 1, Appli
8	28.6	27.2	2616	4 US-09-220-132-6	Sequence 1, Appli
9	27.6	26.3	1001	4 US-09-641-338-387	Sequence 387, App
10	27.6	26.3	1001	4 US-09-641-338-387	Sequence 388, App
11	27.6	26.3	1001	4 US-09-641-338-387	Sequence 388, App
12	27.2	25.9	1665	4 US-09-641-638-389	Sequence 389, App
13	27	25.7	925	1 US-08-850-117-1	Sequence 1, Appli
14	27	25.7	925	2 US-09-008-181-1	Sequence 1, Appli
15	27	25.7	1311	2 US-08-530-569B-1	Sequence 1, Appli
16	25.8	24.6	1710	1 US-07-903-103-3	Sequence 3, Appli
17	25.8	24.6	1710	1 US-08-044-619A-3	Sequence 3, Appli
18	25.8	24.6	1710	1 US-08-283-911-3	Sequence 3, Appli
19	25.8	24.6	1710	1 US-08-245-500A-4	Sequence 4, Appli
20	25.8	24.6	1710	1 US-08-390-546-4	Sequence 4, Appli
21	25.8	24.6	1710	1 US-08-390-479A-4	Sequence 4, Appli
22	25.8	24.6	1710	1 US-08-557-393-4	Sequence 4, Appli
23	25.8	24.6	1710	1 US-08-390-516C-4	Sequence 4, Appli
24	25.8	24.6	1710	1 US-08-390-517A-4	Sequence 4, Appli
25	25.8	24.6	1710	1 US-08-390-515A-4	Sequence 4, Appli
26	25.8	24.6	1710	2 US-08-801-718-4	Sequence 4, Appli
27	25.8	24.6	1710	3 US-09-073-567-12	Sequence 12, Appli

#### ALIGNMENTS

c	28	25.8	24.6	1710	4 US-09-170-159A-4
c	29	25.8	24.6	1710	4 US-09-180-118-45
c	30	25.6	24.4	167450	4 US-09-345-982-1
c	31	25.4	24.2	4065	4 US-09-016-434-1105
c	32	25.4	24.2	4739	3 US-08-085-371-1
c	33	25.4	24.2	5596	3 US-09-078-294-5
c	34	25.4	24.2	80246	3 US-09-078-294-4
c	35	25.4	24.2	80595	3 US-09-078-294-3
c	36	25	23.8	948	4 US-09-252-991A-10169
c	37	25	23.8	2310	1 US-08-416-581B-6
c	38	25	23.8	2652	1 US-08-416-581B-7
c	39	25	23.8	2652	1 US-08-416-581B-8
c	40	25	23.8	2869	2 US-08-369-296-11
c	41	25	23.8	2869	2 US-08-852-091-11
c	42	25	23.8	2869	2 US-08-820-054-11
c	43	25	23.8	2869	3 US-08-956-062-11
c	44	25	23.8	2869	3 US-08-956-069-11
c	45	25	23.8	2869	3 US-08-948-247-11

RESULT 1	US-08-200-232-1	/ Sequence 1, Application US/08200232
GENERAL INFORMATION:		
Patent No. 5721349		
APPLICANT: Blaser, Martin J. L.		
TITLE OF INVENTION: VACUOLATING TOXIN DEFICIENT H. PYLORI		
TITLE OF INVENTION: AND RELATED METHODS		
NUMBER OF SEQUENCES: 18		
CORRESPONDENCE ADDRESS:		
ADDRESSEE: NEEDS & ROSENBERG P.C.		
STREET: 127 Peachtree Street, Suite 1200		
CITY: Atlanta		
STATE: Georgia		
ZIP: 30303		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: PatentIn Release #1.0, Version #1.25		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/200,232		
FILING DATE:		
CLASSIFICATION: 424		
ATTORNEY/AGENT INFORMATION:		
NAME: Spratt, Gwendolyn D.		
REGISTRATION NUMBER: 36 016		
REFERENCE/DOCKET NUMBER: 2200 .023		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: 404/688-0770		
TELEFAX: 404/688-9880		
SEQUENCE CHARACTERISTICS:		
LENGTH: 4042 base pairs		
TYPE: nucleic acid		
STRANDBENDNESS: double		
TOPOLOGY: linear		
MOLECULE TYPE: DNA (genomic)		
FEATURE:		
NAME/KEY: CDS		
LOCATION: 101..3964		
US-08-200-232-1		
Query Match 83.2%; Best Local Similarity 89.5%; Pred. No. 1e-21; Length 4042;		
Matches 94%; Conservative 0%; Mismatches 11%; Indels 0%; Gaps 0%;		
QY 1 CCCTTTAGTTCTCGCTTATGGGTAGCATCACACAAAAAGTC 60		

```

RESULT 2 PCT-US95-02219-1
; Sequence 1, Application PC/TUS9502219.9
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYORI
; TITLE OF INVENTION: AND RELATED METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200 . 023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SBQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4042 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..3964
PCT-US95-02219-1

Query Match          83.2%; Score 87.4; DB 5; Length 4042;
Best Local Similarity 85.5%; Pred. No. 1e-21;
Matchas 94; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
; Sequence 1, Application PC/TUS9502219A
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Tummuri, Murali KR
; APPLICANT: Cao, Ping
; APPLICANT: Thompson, Stuart A.

Query Match          83.2%; Score 87.4; DB 5; Length 4042;
Best Local Similarity 85.5%; Pred. No. 1e-21;
Matchas 94; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
; Sequence 1, Application PC/TUS9502219A-1
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Tummuri, Murali KR
; APPLICANT: Cao, Ping
; APPLICANT: Thompson, Stuart A.

Db      136 CCCTTGTGTTCTCGGTTAGGGGGTATGGTAGCATCACACCAAAAGTCGA 60
Db      136 CCCTTGTGTTCTCGGTTAGGGGGTATGGTAGCATCACACCAAAAGTCGA 195
Db      196 TGCGCCCTTTAACACCGTATCCAGCATTGTTGGGG 105
Db      196 TGCGCCCTTTAACACCGTATCCAGCATTGTTGGGG 240

RESULT 3 PCT-US95-02219A-1
; Sequence 1, Application PC/TUS9502219A
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Tummuri, Murali KR
; APPLICANT: Cao, Ping
; APPLICANT: Thompson, Stuart A.

```

APPLICANT: Blaser, Martin J. VACUOLATING TOXIN-DEFICIENT H. PYLORI  
 TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: NEEDS & ROSENBERG P.C.  
 STREET: 127 Peachtree Street, Suite 1200  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30303  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/02219A  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Spratt, Gwendolyn D.  
 REGISTRATION NUMBER: 36, 016  
 REFERENCE/DOCKET NUMBER: 2200-0.023  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 404/688-0770  
 TELEFAX: 404/688-9880  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4042 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 101..3964  
 PCT-US95-02219A-1

	Query Match	Score	Length	DB	Match	Best Local Similarity	Pred.	No.	Indels
Qy	1 CCCCTAGTTCTCTCGCTTATTAGTCGGCTTATTGTCAGCATCACACAC	83.2%	404	5;	94;	89.5%	1e-21;	0;	Mismatches
Db	136 CCCCTGGTTCTCTGGTTATTAGGGATGTGAGATCACCGGG	89.5%	105	5;	94;	Conservative	0;	0;	
Qy	61 TGCGCCCTCTTACACCTGATCATCCGCCATTGTCGGGG	87.4	105	5;	94;				
Db	196 TGCCGCCCTTACACCTGATCATCCGCCATTGTCGGGG	87.4	240	5;	94;				

RESULT 4  
 US-08-470-260-2  
 / Sequence 2, Application US/08470260  
 / Patent No. 6077706  
 / GENERAL INFORMATION:  
 / APPLICANT: Covacci, Antonello  
 / APPLICANT: Bugnoli, Massimo  
 / APPLICANT: Macchia, Giovanni  
 / APPLICANT: Rappuoli, Rino  
 / TITLE OF INVENTION: Helicobacter pylori Proteins Useful  
 / TITLE OF INVENTION: for Vaccines and Diagnostics  
 / NUMBER OF SEQUENCES: 7  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Chiron Corporation  
 / STREET: 4560 Horton Street  
 / CITY: Emeryville  
 / STATE: California  
 / COUNTRY: USA  
 / ZIP: 94608-2916  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/470,260  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/256,848  
 FILING DATE: 21-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McCullung, Barbara G.  
 REGISTRATION NUMBER: 33,113  
 REFERENCE/DOCKET NUMBER: 0316.001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 601-7708  
 TELEFAX: (510) 655-3542  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3960 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-470-260-2

Query Match Score 81.7%; DB 3; Length 3960;  
 Best Local Similarity 88.6%; Pred. No. 3.8e-21;  
 Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

y 1 CCCTTAGTTCTCGCTTAGTCGGTTATGGTCAACCCACAAAAAAGTCA 60  
 b 53 CCCCTGGTCTCGCTTAGGAGATTGTAGATCACCCGAACAAAGTCA 112

y 61 TGCAGCCCTCTTACAACCGTATTCAGCATTGGGGGG 105  
 b 113 TGCCGCCCTTTCAACCGTATTCAGCATTGGGGGG 157

RESULT 5  
 US-08-471-491-2  
 Sequence 2, Application US/08471491B  
 PATENT NO. 6090611  
 GENERAL INFORMATION:  
 APPLICANT: Covacci, Antonello  
 APPLICANT: Bugnoli, Massimo  
 APPLICANT: Telford, John  
 APPLICANT: Macchia, Giovanni  
 APPLICANT: Rappuoli, Rino  
 TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And  
 FILE REFERENCE: CHIR0044  
 CURRENT APPLICATION NUMBER: US/08/471,491B  
 CURRENT FILING DATE: 1995-06-06  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2  
 LENGTH: 3960  
 TYPE: DNA  
 ORGANISM: Helicobacter pylori  
 US-08-471-491-2

Query Match Score 81.7%; DB 3; Length 3960;  
 Best Local Similarity 88.6%; Pred. No. 3.1e-21;  
 Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

y 1 CCCTTAGTTCTCGCTTAGTCGGTTATGGTCAACCCACAAAAAAGTCA 60  
 b 53 CCCCTGGTCTCGCTTAGGAGATTGTAGATCACCCGAACAAAGTCA 112

y 61 TGCAGCCCTCTTACAACCGTATTCAGCATTGGGGGG 105

RESULT 6  
 US-08-466-662-2  
 Sequence 2, Application US/08466662B  
 PATENT NO. 6130059  
 GENERAL INFORMATION:  
 APPLICANT: Covacci, Antonello  
 APPLICANT: Bugnoli, Massimo  
 APPLICANT: Telford, John  
 APPLICANT: Macchia, Giovanni  
 APPLICANT: Rappuoli, Rino  
 TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And  
 FILE REFERENCE: CHIR0057  
 CURRENT APPLICATION NUMBER: US/08/466,662B  
 CURRENT FILING DATE: 1995-06-06  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2  
 LENGTH: 3960  
 TYPE: DNA  
 ORGANISM: Helicobacter pylori  
 US-08-466-662-2

Query Match Score 81.7%; DB 3; Length 3960;  
 Best Local Similarity 88.6%; Pred. No. 3.8e-21;  
 Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTCTCGCTTAGTCGGTTATGGTCAACCCACAAAAAAGTCA 60  
 Db 53 CCCCTGGTCTCGCTTAGGAGATTGTAGATCACCCGAACAAAGTCA 112

Qy 61 TGCAGCCCTCTTACAACCGTATTCAGCATTGGGGGG 105  
 Db 113 TGCCGCCCTTTCAACCGTATTCAGCATTGGGGGG 157

RESULT 7  
 US-08-295-643-1  
 Sequence 1, Application US/08295643  
 PATENT NO. 5859219  
 GENERAL INFORMATION:  
 APPLICANT: COVER, TIMOTHY L.  
 APPLICANT: BLASER, MARTIN J.  
 TITLE OF INVENTION: PURIFIED VACUOLATING TOXIN FROM  
 HELICOBACTER PYLORI AND METHODS TO USE SAME  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: NEEDLE & ROSENBERG, P.C.  
 STREET: Suite 1200, 127 Peachtree Street  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30303

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/295,643  
 FILING DATE: 26-AUG-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SPRAATT, GWENDOLYN D.  
 REGISTRATION NUMBER: 36,016  
 REFERENCE DOCKET NUMBER: 2200.025  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 404/688-0770  
 TELEX: 404/688-3880  
 INFORMATION FOR SEQ ID NO: 1:

Query Match Score 81.7%; DB 3; Length 3960;  
 Best Local Similarity 88.6%; Pred. No. 3.1e-21;  
 Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

y 1 CCCTTAGTTCTCGCTTAGTCGGTTATGGTCAACCCACAAAAAAGTCA 60  
 b 53 CCCCTGGTCTCGCTTAGGAGATTGTAGATCACCCGAACAAAGTCA 112

y 61 TGCAGCCCTCTTACAACCGTATTCAGCATTGGGGGG 105

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1412 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 US-08-295-643-1

Query Match 37.5% Score 39 4; DB 2; Length 1412;  
 Best Local Similarity 97.6%; Pred. No. 9 ; e-05;  
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-220-132-6/C  
 Sequence 6, Application US/09220132  
 Patent No. 6506607

GENERAL INFORMATION:  
 APPLICANT: Shyan, Andrew W.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER  
 FILE REFERENCE: 07324-74001  
 CURRENT APPLICATION NUMBER: US/09/220,132  
 CURRENT FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 60/019,303  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: US 60/068,821  
 PRIOR FILING DATE: 1997-12-24  
 NUMBER OF SEQ ID NOS: 191  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 6  
 LENGTH: 2616  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-220-132-6

RESULT 8  
 Query Match 37.5% Score 39 4; DB 2; Length 1412;  
 Best Local Similarity 97.6%; Pred. No. 9 ; e-05;  
 Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 GGCTCTTACAACCGTATCATCCAGCCATTGTTGGGG 105  
 Db 1 GCCTTTAAACCGTATCATCCAGCCATTGTTGGGG 41

Query Match 26.3% Score 27.6; DB 4; Length 1001;  
 Best Local Similarity 67.2%; Pred. No. 1,3;  
 Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 CCCTTAGTTCTTCGCTTATGGGTATTGTCAGCATCACCAAAAGT 58  
 Db 410 CCTGTCATTTAGGTAGTGTGCTATGTCATAATGTCATAATGTCATAAGT 353

RESULT 10  
 US-09-641-638-388/C  
 Sequence 388, Application US/09641638  
 Patent No. 6431648

GENERAL INFORMATION:  
 APPLICANT: Blumentfeld, Marta  
 APPLICANT: Bougueret, Lydie  
 APPLICANT: Chumakov, Illya  
 APPLICANT: Cohen, Annick  
 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
 FILE REFERENCE: GENSET 051CPI  
 CURRENT APPLICATION NUMBER: US/09/641,638  
 CURRENT FILING DATE: 2000-08-16  
 PRIOR APPLICATION NUMBER: US 09/502,330  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: US 60/133,200  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: US 09/275,267  
 PRIOR FILING DATE: 1999-03-23  
 PRIOR APPLICATION NUMBER: US 60/119,917  
 NUMBER OF SEQ ID NOS: 1304  
 SOFTWARE: Patent .pm  
 SEQ ID NO: 388

LENGTH: 1001

TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: allele

OTHER INFORMATION: 12-886-195 : polymorphic base T or C  
 NAME/KEY: misc\_binding  
 LOCATION: 501

OTHER INFORMATION: 12-886-348 : polymorphic base T or C  
 NAME/KEY: misc\_binding  
 LOCATION: 481-500

OTHER INFORMATION: 12-886-348.mis1, potential  
 OTHER INFORMATION: 12-886-348.mis1

RESULT 9  
 US-09-641-638-387/C  
 Sequence 387, Application US/09641638  
 Patent No. 6432648

GENERAL INFORMATION:  
 APPLICANT: Blumentfeld, Marta  
 APPLICANT: Bougueret, Lydie  
 APPLICANT: Chumakov, Illya  
 APPLICANT: Cohen, Annick  
 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
 FILE REFERENCE: GENSET 051CPI  
 CURRENT APPLICATION NUMBER: US/09/641,638  
 CURRENT FILING DATE: 2000-08-16  
 PRIOR APPLICATION NUMBER: US 09/502,330  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: US 60/133,200  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: US 09/275,267  
 PRIOR FILING DATE: 1999-03-23  
 PRIOR APPLICATION NUMBER: US 60/119,917  
 NUMBER OF SEQ ID NOS: 1304  
 SOFTWARE: Patent .pm  
 SEQ ID NO: 388

LENGTH: 1001

TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: allele

OTHER INFORMATION: 12-886-195 : polymorphic base T or C  
 NAME/KEY: misc\_binding  
 LOCATION: 501

OTHER INFORMATION: 12-886-348 : polymorphic base T or C  
 NAME/KEY: misc\_binding  
 LOCATION: 481-500

OTHER INFORMATION: 12-886-348.mis1, potential  
 OTHER INFORMATION: 12-886-348.mis1

```

NAME/KEY: misc_binding
LOCATION: 502..521
OTHER INFORMATION: 12-886-348.mi82, potential complement
NAME/KEY: primer_bind
LOCATION: 827..847
OTHER INFORMATION: upstream amplification primer, complement
NAME/KEY: primer_bind
LOCATION: 399..419
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-886-348 Potential probe
JS-09-641-638-388

Query Match          Score 26.3%;  DB 4;  Length 1001;
Best Local Similarity 67.2%;  Pred. No. 1..3;
Matches   39;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
                1 CCCCTTAGTTCTCGCTTAGGGTTATGGTACCATCACAAAGT 58
                | | | | | | | | | | | | | | | | | | | | | | | | |
                563 CTCGCACTTAGGTAGCTGAATGTTGCTTAATCATCTCACAGAGT 506

RESULTS 11
JS-09-641-638-389/C
Sequence 389, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenthal, Marta
APPLICANT: Bouquelaret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET_051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent-PM
SEQ ID NO 389
LENGTH: 1001
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-887-201 : polymorphic base G or A
NAME/KEY: misc_binding
LOCATION: 481..500
OTHER INFORMATION: 12-887-201.mi81, potential complement
NAME/KEY: misc_binding
LOCATION: 502..521
OTHER INFORMATION: 12-887-201.mi82, potential complement
NAME/KEY: primer_bind
LOCATION: 683..701
OTHER INFORMATION: upstream amplification primer, complement
NAME/KEY: primer_bind
LOCATION: 184..204
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-887-201 potential probe
JS-09-641-638-389

Query Match          Score 26.3%;  DB 4;  Length 1001;

```

ADDRESSEE: SmithKline Beecham Corporation  
 CITY: 709 Swedeland Road  
 STATE: King of Prussia  
 COUNTRY: USA  
 ZIP: 19406-0939  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/850,117  
 FILING DATE: 01-MAY-97  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 9609020.4  
 FILING DATE: 01-MAY-96  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gimmi, Edward R  
 REGISTRATION NUMBER: 38,891  
 PREFERENCE/DOCKET NUMBER: P31479  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-270-4478  
 TELEX: 610-270-5090  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 925 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 US-08-850-117-1

RESULT 14  
 US-09-008-181-1/c  
 Sequence 1, Application US/09008181  
 GENERAL INFORMATION:  
 APPLICANT: Wallis, Nicola  
 TITLE OF INVENTION: No. 5919904e1 Compounds  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 STREET: 709 Swedeland Beecham Corporation  
 CITY: King of Prussia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19406-0939  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/008,181  
 PRIORITY APPLICATION DATA:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/850,117  
 FILING DATE: 01-MAY-97  
 APPLICATION NUMBER: 9509020.4  
 FILING DATE: 01-MAY-96  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gimmi, Edward R  
 REGISTRATION NUMBER: 38,891  
 PREFERENCE/DOCKET NUMBER: P31479  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-270-4478  
 TELEX: 610-270-5090  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 925 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 US-09-008-181-1

RESULT 15  
 US-08-530-569B-1  
 Sequence 1, Application US/08530569B  
 GENERAL INFORMATION:  
 PATENT NO. 5933526  
 APPLICANT: Gaugler, Beatrice  
 APPLICANT: van den Eynde, Benoit  
 APPLICANT: Schrier, Peter  
 APPLICANT: Brouwenstijn, Nathalie  
 APPLICANT: Boon-Fauvel, Thierry  
 TITLE OF INVENTION: Isolated Peptides which  
 TITLE OF INVENTION: Isolated PAGE-1 Derived Peptides which  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Complex with HLA-B7 Molecules and Uses Thereof  
 CITY: Federal Reserve Plaza, 600 Atlantic Avenue  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/530,569B  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gates, Edward R.  
 REGISTRATION NUMBER: 31,616  
 PREFERENCE/DOCKET NUMBER: L0461/7002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-720-3500  
 TELEFAX: 617-720-2441  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1311 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
S-08-530-569B-1

Query	Match	Score	Length
Y	14 CTCGCTTAGTGGGTATTGGTAGCATCACACAAAAAGTCATGCTGCCTTCRTT	27	1311;
b	338 CCCCTTCTGAGTAATGACTGACCAATCTAAAATCCAGATGTCATCGC	62.7	73
Y	74 ACACCCG	80	
b	398 ACACCCG	404	

Best Local Similarity 62.7%; Pred. No. 2.4; Mismatches 0;保守性 Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

search completed: January 13, 2004, 02:56:33  
db time : 64 Secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

run on: January 13, 2004, 01:22:01 ; Search time 305 Seconds  
 (without alignments)  
 1195.490 Million cell updates/sec

Title: US-10-035-978A-126

Effect score: 105

Sequence: 1 ccctttatgttctcgctt.....attccagccatgtgggg 105

Coring table: IDENTITY\_NUC Gapext 1.0

Searched: 2276164 seqs, 1736306516 residues

Total number of hits satisfying chosen parameters: 4552328

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0<sup>t</sup>  
 Listing first 45 summaries

Databases:

- 1: Published Applications NA: \*
- 2: /cgn2\_6\_ptodata/1/pubpna/us07\_pubcomb.seq:\*
- 3: /cgn2\_6\_ptodata/1/pubpna/us07\_pubseq:\*
- 4: /cgn2\_6\_ptodata/1/pubpna/us07\_pubcomb.seq:\*
- 5: /cgn2\_6\_ptodata/1/pubpna/us07\_pubseq:\*
- 6: /cgn2\_6\_ptodata/1/pubpna/pctus\_pubcomb.seq:\*
- 7: /cgn2\_6\_ptodata/1/pubpna/us08\_pubseq:\*
- 8: /cgn2\_6\_ptodata/1/pubpna/us08\_pubcomb.seq:\*
- 9: /cgn2\_6\_ptodata/1/pubpna/us09\_pubcomb.seq:\*
- 10: /cgn2\_6\_ptodata/1/pubpna/us09b\_pubcomb.seq:\*
- 11: /cgn2\_6\_ptodata/1/pubpna/us09c\_pubcomb.seq:\*
- 12: /cgn2\_6\_ptodata/1/pubpna/us09\_new\_pub.seq:\*
- 13: /cgn2\_6\_ptodata/1/pubpna/us09\_new\_pub.seq:\*
- 14: /cgn2\_6\_ptodata/1/pubpna/us10\_pubcomb.seq:\*
- 15: /cgn2\_6\_ptodata/1/pubpna/us10b\_pubcomb.seq:\*
- 16: /cgn2\_6\_ptodata/1/pubpna/us10\_new\_pub.seq:\*
- 17: /cgn2\_6\_ptodata/1/pubpna/us60\_new\_pub.seq:\*
- 18: /cgn2\_6\_ptodata/1/pubpna/us60\_pubcomb.seq:\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	105	100.0	105	13	US-10-035-978A-126 J.2
2	105	100.0	105	13	US-10-035-978A-127
3	105	100.0	105	13	US-10-035-978A-126
4	105	100.0	105	13	US-10-035-978A-127
5	103.4	98.5	105	13	US-10-035-978A-128
6	103.4	98.5	105	13	US-10-035-978A-128
7	101.8	97.0	105	13	US-10-035-978A-132
8	101.8	97.0	105	13	US-10-035-978A-132
9	100.2	95.4	105	13	US-10-035-978A-129
10	100.2	95.4	105	13	US-10-035-978A-131
11	100.2	95.4	105	13	US-10-035-978A-131
12	100.2	95.4	105	13	US-10-035-978A-131
13	100.2	95.4	105	13	US-10-035-978A-131
14	100.2	95.4	105	13	US-10-035-978A-131
15	99.4	94.7	105	13	US-10-035-978A-130

Result 1  
 US-10-035-978A-126 Application US/10035978A

GENERAL INFORMATION:  
 Publication No. US200301658601  
 Sequence 126, Application US/10035978A  
 Quint, Wilhelmus  
 Van Doorn, Leendert  
 TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION  
 AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN  
 TITLE OF INVENTION: BIOLOGICAL SAMPLES  
 FILE REFERENCE: INN02\_001C1  
 CURRENT APPLICATION NUMBER: US/10/035\_978A  
 PRIORITY FILING DATE: 2001-12-21  
 PRIORITY APPLICATION NUMBER: US/10/284\_725  
 PRIORITY FILING DATE: 1999-04-16  
 PRIORITY FILING DATE: 1997-09-09  
 PRIORITY APPLICATION NUMBER: EP 97870133.2  
 PRIORITY FILING DATE: 1996-10-16  
 NUMBER OF SEQ ID NOS: 280  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 126  
 LENGTH: 105  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence  
 US-10-035-978A-126

Query Match 100.0%; Score 105; DB 13;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-28;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCCTTGTGTTCTCCCTTAGGGTTAGGTCTACCAAAAGTCA 60  
 1 CCCTTGTGTTCTCCCTTAGGGTTAGGTCTACCAAAAGTCA 60

Qy 1 CGCTTGTGTTCTCCCTTAGGGTTAGGTCTACCAAAAGTCA 60  
 Db 1 CGCTTGTGTTCTCCCTTAGGGTTAGGTCTACCAAAAGTCA 60

Qy 61 TGTCGCCCTCTTACACCGTATCATTCAGCCATTGTTGGGG 105



REGISTRATION NUMBER: 34,115  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (949) 760-404  
 TELEX/FAX: (949) 760-935  
 INFORMATION FOR SEQ ID NO: 127:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 105 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 127;

Query Match 100.0%; Score 105; DB 13; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-28;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2Y      1 CCCTTTAGTTCTCGCTTATGGGGTATTGGTAGCATCACCAAAAGTCA 60
       1 CCTTTAGTTCTCGCTTATGGGGTATTGGTAGCATCACCAAAAGTCA 60
bY      61 TGCAGCTCTTTAACCCGTGATCATTCAGCATTGTTGGGG 105
bY      61 TGCAGCTCTTTAACCCGTGATCATTCAGCATTGTTGGGG 105

```

:RESULT 5

Sequence 128. Application US/10035978A

GENERAL INFORMATION:

APPLICANT: Quint, Wilhelmus

TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN

TITLE OF INVENTION: BIOLOGICAL SAMPLES

FILE REFERENCE: INNOG2.001C1

CURRENT APPLICATION NUMBER: US/10/035,978A

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: EP 97870133.2

PRIOR FILING DATE: 1997-09-09

PRIOR APPLICATION NUMBER: EP 96870131.8

PRIOR FILING DATE: 1996-10-16

NUMBER OF SEQ ID NOS: 280

SOFTWARE: FastSBQ for Windows Version 4.0

SEQ ID NO: 128

LENGTH: 105

TYPE: DNA

FEATURE: Artificial Sequence

OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence

S-10-035-978A-128

Query Match 98.5%; Score 103.4; DB 13; Length 105;

Best Local Similarity 99.0%; Pred. No. 2.6e-27;

Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 98.5%; Score 103.4; DB 13; Length 105;

Best Local Similarity 99.0%; Pred. No. 2.6e-27;

Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7

Query Match 98.5%; Score 103.4; DB 13; Length 105;

Best Local Similarity 99.0%; Pred. No. 2.6e-27;

Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-035-978A-132

; Sequence 132. Application US/10035978A

; Publication No. US0030165860A1

; GENERAL INFORMATION:

; APPLICANT: Van Doorn, Leendert

; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION

; AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN

TITLE OF INVENTION: BIOLOGICAL SAMPLES  
 FILE REFERENCE: INNOG2.001C1  
 CURRENT APPLICATION NUMBER: US/10/035, 978A  
 CURRENT FILING DATE: 2001-12-21  
 PRIOR APPLICATION NUMBER: US/030175746A1  
 PRIOR FILING DATE: 1999-04-16  
 PRIOR APPLICATION NUMBER: EP 97870133.2  
 PRIOR FILING DATE: 1997-09-09  
 PRIOR APPLICATION NUMBER: EP 96870131.8  
 PRIOR FILING DATE: 1996-10-16  
 NUMBER OF SEQ ID NOS: 280  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 132  
 LENGTH: 105  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Helicobacter pylori vaca nucleic acid sequence  
 US-10-035-978A-132

Query Match	97.0%	Score 101.8;	DB 13;	Length 105;
Best Local Similarity	98.1%	Pred. No. 9.6e-27;	0; Mismatches 2;	Indels 0; Gaps 0;
Matches	103;	Conservative		

Qy 1 CCCCTTAACTTCCTCGCTTAGTCGGTTATTGGTCAGCATCACCCACAAAAAGTCA 60  
 Db 1 CCCCTTAACTTCCTCGCTTAGTCGGTTATTGGTCAGCATCACCCACAAAAAGTCA 60

RESULT 9  
 US-10-035-978A-129

Sequence 129, Application US/10035978A	
Publication No. US20030165860A1	
GENERAL INFORMATION:	
APPLICANT: Quint, Wilhelmus	
APPLICANT: van Doorn, Leendert	
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION	
OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN	
OTHER INFORMATION: BIOMATERIALS	
FILE REFERENCE: INNOG2.001C1	
CURRENT APPLICATION NUMBER: US/10/035, 978A	
PRIOR APPLICATION NUMBER: 09/284, 725	
PRIOR FILING DATE: 1999-04-16	
PRIOR APPLICATION NUMBER: EP 97870133.2	
PRIOR FILING DATE: 1997-09-09	
PRIOR APPLICATION NUMBER: EP 96870131.8	
PRIOR FILING DATE: 1996-10-16	
NUMBER OF SEQ ID NOS: 280	
SOFTWARE: FastSEQ for Windows Version 4.0	
SEQ ID NO: 129	
LENGTH: 105	
TYPE: DNA	
ORGANISM: Artificial Sequence	
FEATURE:	

OTHER INFORMATION: Helicobacter pylori vaca nucleic acid sequence

US-10-035-978A-132

Query Match	95.4%	Score 100.2;	DB 13;	Length 105;
Best Local Similarity	97.1%	Pred. No. 3.6e-26;	0; Mismatches 3;	Indels 0; Gaps 0;
Matches	102;	Conservative		

Qy 1 CCCCTTAACTTCCTCGCTTAGTCGGTTATTGGTCAGCATCACCCACAAAAAGTCA 60  
 Db 1 CCCCTTAACTTCCTCGCTTAGTCGGTTATTGGTCAGCATCACCCACAAAAAGTCA 60

RESULT 10  
 US-10-035-978A-131

Sequence 131, Application US/10035978A	
Publication No. US20030165860A1	
GENERAL INFORMATION:	
APPLICANT: Quint, Wilhelmus	
APPLICANT: Altman, Daniel E.	
REGISTRATION NUMBER: 34,115	
REFERENCE/DOCKET NUMBER: INNOG2.001APC	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: (949) 760-0404	
TELEFAX: (949) 760-9395	

APPLICANT: Van Doorn, Leendert  
 TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION  
 TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEAR ACIDS IN  
 TITLE OF INVENTION: BIOLOGICAL SAMPLES  
 FILE REFERENCE: INNOG2.001C1  
 CURRENT APPLICATION NUMBER: US/10/035, 978A  
 CURRENT FILING DATE: 2001-12-21  
 PRIORITY FILING DATE: 1999-04-16  
 PRIORITY APPLICATION NUMBER: EP 97870133.2  
 PRIORITY FILING DATE: 1997-09-09  
 PRIORITY APPLICATION NUMBER: EP 96870131.8  
 PRIORITY FILING DATE: 1996-10-16  
 NUMBER OF SEQ ID NOS: 280  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO: 131  
 LENGTH: 105  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence  
 IS-10-035-978A-131

Query Match 95.4%; Score 100.2; DB 13; Length 105;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

y 1 CCCCTTAGTTCTCGCTTAGGGATTGGTCACTACACCAAAAGTCA 60  
 b 1 CCCCTTAGTTCTCGCTTAGGGATTGGTCACTACACCGAAAAAGTCA 60

y 61 TGCTGCCCTTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 b 61 TGCCGCCCTTTACAACCGTGAATTCGGCCATTGTGGGG 105

RESULT 11  
 Sequence 133 Application US/10/035918A  
 Publication No. US20030163860A1  
 GENERAL INFORMATION:  
 APPLICANT: Quint, Wilhelmus  
 APPLICANT: Van Doorn, Leendert  
 TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION  
 TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEAR ACIDS IN  
 TITLE OF INVENTION: BIOLOGICAL SAMPLES  
 FILE REFERENCE: INNOG2.001C1  
 CURRENT APPLICATION NUMBER: US/10/035, 978A  
 CURRENT FILING DATE: 2001-12-21  
 PRIORITY FILING DATE: 1999-04-16  
 PRIORITY APPLICATION NUMBER: EP 97870133.2  
 PRIORITY FILING DATE: 1997-09-09  
 PRIORITY APPLICATION NUMBER: EP 96870131.8  
 PRIORITY FILING DATE: 1996-10-16  
 NUMBER OF SEQ ID NOS: 280  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO: 133  
 LENGTH: 105  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence  
 IS-10-035-978A-133

Query Match 95.4%; Score 100.2; DB 13; Length 105;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

y 1 CCCCTTAGTTCTCGCTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 b 1 CCCCTTAGTTCTCGCTTACAACCGTGAATTCAGCCATTGTGGGG 105

RESULT 13  
 Sequence 131 Application US/10/0263594  
 ; Sequence 131, Application US/10/0263594

Qy 61 TGCTGCCCTTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 Db 61 TGCCGCCCTTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 RESULT 12  
 US-10-263-594-129  
 ; Sequence 129, Application US/10263594  
 Publication No. US20030175746A1  
 GENERAL INFORMATION:  
 APPLICANT: Quint, Wilhelmus  
 Van Doorn, Leendert  
 TITLE OF INVENTION: Probes, methods and kits for detection and  
 typing of Helicobacter pylori nucleic acids in biological  
 samples.  
 NUMBER OF SEQUENCES: 280  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Knobbe, Martens, Olson & Bear, LLP  
 CITY: 620 Newport Center Drive, 16th Floor  
 STATE: Newport Beach  
 COUNTRY: CA  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/263, 594  
 FILING DATE: 02-Oct-2002  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP96/870131.8  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: EP96/870131.8  
 FILING DATE: 16-Oct-1996  
 APPLICATION NUMBER: PCT/EP97/05614  
 FILING DATE: 10-Oct-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Altman, Daniel E.  
 REGISTRATION NUMBER: 34,115  
 REFERENCE/DOCKET NUMBER: INNOG2.001APC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (949) 760-0404  
 TELEFAX: (949) 760-3995  
 INFORMATION FOR SEQ ID NO: 129:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 105 base pairs  
 TYPE: nucleic acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
 US-10-263-594-129  
 Query Match 95.4%; Score 100.2; DB 13; Length 105;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 CCCCTTAGTTCTCGCTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 Db 1 TGCTGCCCTTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 Qy 61 TGCTGCCCTTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 Db 61 TGCCGCCCTTTACAACCGTGAATTCAGCCATTGTGGGG 105  
 RESULT 13  
 Sequence 131 Application US/10263594  
 ; Sequence 131, Application US/10/0263594

Publication No. US20030175746A1  
 GENERAL INFORMATION:  
 APPLICANT: Quint, Wilhelmus  
 Van Doorn, Leendert  
 TITLE OF INVENTION: Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples.

NUMBER OF SEQUENCES: 280

CORRESPONDENCE ADDRESS:  
 ADDRESS: Knobbe, Martens Olson & Bear, LLP  
 STREET: 620 Newport Center Drive, 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/263,594  
 FILING DATE: 02-OCT-2002  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/09/284,725  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: EP96/870131.8  
 FILING DATE: 16-OCT-1996  
 APPLICATION NUMBER: PCT/EP97/05614  
 FILING DATE: 10-OCT-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Altman, Daniel E.  
 REGISTRATION NUMBER: 34,115  
 REFERENCE/DOCKET NUMBER: INNOG2.001APC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (949) 760-0404  
 TELEFAX: (949) 760-9395

INFORMATION FOR SEQ ID NO: 133:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 105 base pairs  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 SEQUENCE DESCRIPTION: SEQ ID NO: 133:  
 US-10-263-594-133

Query Match 95.4%; Score 100.2; DB 13; Length 105;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60  
 Db 1 CCCTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60

Query Match 95.4%; Score 100.2; DB 13; Length 105;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60  
 Db 1 CCCTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60

RESULT 14  
 US-10-263-594-133  
 Sequence 133, Application US/10263594  
 Publication No. US20030175746A1  
 GENERAL INFORMATION:  
 APPLICANT: Quint, Wilhelmus  
 Van Doorn, Leendert  
 TITLE OF INVENTION: Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples.

NUMBER OF SEQUENCES: 280

CORRESPONDENCE ADDRESS:  
 ADDRESS: Knobbe, Martens Olson & Bear, LLP  
 STREET: 620 Newport Center Drive, 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/263,594  
 FILING DATE: 02-OCT-2002  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/09/284,725  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: EP96/870131.8  
 FILING DATE: 16-OCT-1996  
 APPLICATION NUMBER: PCT/EP97/05614  
 FILING DATE: 10-OCT-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Altman, Daniel E.  
 REGISTRATION NUMBER: 34,115  
 REFERENCE/DOCKET NUMBER: INNOG2.001APC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (949) 760-0404  
 TELEFAX: (949) 760-9395

INFORMATION FOR SEQ ID NO: 133:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 105 base pairs  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 SEQUENCE DESCRIPTION: SEQ ID NO: 133:  
 US-10-263-594-133

Query Match 95.4%; Score 100.2; DB 13; Length 105;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60  
 Db 1 CCCCTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60

Query Match 95.4%; Score 100.2; DB 13; Length 105;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60  
 Db 1 CCCCTTAGTTCTCGCTTATGGGGTTATGGTCACTACACAAAGTCA 60

RESULT 15  
 US-10-035-978A-130  
 Sequence 130, Application US/10035978A  
 Publication No. US2003016860A1  
 GENERAL INFORMATION:  
 APPLICANT: Quint, Wilhelmus  
 Van Doorn, Leendert  
 TITLE OF INVENTION: Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples.

NUMBER OF SEQUENCES: 280

NUMBER OF SEQ ID NOS: 280  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 130  
LENGTH: 105  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence  
'S-10-035-978a-130

Query	Match	94.7%	Score 99.4;	DB 13;	Length 105;
Best Local Similarity	96.2%	Pred. No. 7.1e-26;	Mismatches	0;	Gaps 0;
Matches	101;	Conservative	1;	Indels	0;
Y	1	CCCTTAGTTCTCGCTTAGGGGTATTGGTCAAGATCACACAAAGTC	60		
ib	1	CCCTTAGTTCTCGCTTAGGGGTATTGGTCAAGATCACACAAAGTC	60		
Y	61	TGCCTCCCTTTAACCTGATTTCAACCTGATTTCAACCTGATTTG	105		
ib	61	TGCCTCCCTTTCAACCTGATTTCAACCTGATTTCAACCTGATTTG	105		

Search completed: January 13, 2004, 03:01:51  
Job time : 306 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

TITLE	Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater Pufferfish Tetraodon nigroviridis	FEATURES Source	call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com High quality sequence stop: 431.
JOURNAL	Genome Res. 10 (7), 939-949 (2000)	Location/Qualifiers	1..549
PUBLMED	20359837	/organism="Glycine max"	
REFERENCE	10899143 (bases 1 to 691)	/mol type="mRNA"	
AUTHORS	Genoscope	/db Xref="taxon:3847"	
TITLE	Direct Submission	/clone="SOYBEAN CLONE ID: Gm-01066-4401"	
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequenage : BP 191 91065 EVRY cedex - FRANCE (E-mail : bsegref@genoscope.cns.fr	/tissue type="Leaf and shoot tip, salt stressed, 2 week old seedling"	
COMMENT	- Web : www.genoscope.cns.fr	/lab host="DH10B"	
FEATURES	This sequence is a single read and was generated as part of a large clone alone sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.	/clone lib="Gm-01066"	
SOURCE	1..691	/note="Vector: pBlueScript II SK+; Site 1: EcoRI; Site 2: XbaI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedlings from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a poly (A) tailing kit. A poly (A) sequence with a XbaI restriction site, EcoRI adaptors were ligated to the blunt ended cDNA fragments followed by XbaI digestion. The cDNA fragments were directionally cloned into the EcoRI-XbaI restriction site of the pBlueScript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."	
BASE COUNT	213 a 132 c 120 g 226 t	BASE COUNT ORIGIN	173 a 106 c 114 g 156 t
ORIGIN		Query Match Best Local Similarity Matches	30.5%; Score 32; DB 12; Length 549;
Qy	32.6%; Score 34.2%; DB 29; Length 691;	Best Local Similarity Matches	56.7%; Score 53; DB 12; Length 549;
Db	Pred. No. 1; Mismatches 0; Indels 0; Gaps 0;	0; Mismatches	0; Mismatches 45; Indels 0; Gaps 0;
Qy	4 TTTAGTGTCTCGCTTAAGGGTTATTGGTAGCATCACACAAAAAAAGTCATGC 63	Query Match Best Local Similarity Matches	2 CCTTTAGTTCTCTGGTTTATGGGGTTATGGTCAGCATCACACCAACAAAAAAGTCAT 61
Db	687 TTAAATTGACTCCGGTCTGGATTATTGAGCAGCATGACACACAAAACGTGACG 628	Db	187 CATTGGTTCTCAACTTGGTGTCTCACTGTGCTCACTGTGACGGTTATCRAAAACAGAAGT 246
RESULT	2	Qy	62 GCTGCCCTCTTACACCGTGATCATCCAGCATTGTTGGGG 105
BM085113	BM085113 549 bp mRNA linear EST 19-NOV-2001	Db	247 TGTTCATCTTGTACATGACTATCCTACATTTGAGG 290
LOCUS	BAJ32d05.y1 Gm-cl0106 5' similar to SWLOX2_SOYBN P33417 LIPOXYGENASE-4, mRNA sequence.	RESULT	3
DEFINITION	Gm-cl0106-4401 5' similar to SWLOX2_SOYBN P33417 LIPOXYGENASE-4, mRNA sequence.	LOCUS	BQ294402
ACCESSION	BK085113	DEFINITION	BQ294402..x2 1091 - Immature ear with common ESTs screened by Schmidt lab Zea mays cDNA, mRNA sequence.
VERSION	1	VERSION	BQ294402..1 GI:20803352
KEYWORDS		KEYWORDS	Zea mays
ORGANISM	Glycine max (soybean)	ORGANISM	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytinae; Panicoidea; Magnoliophyta; Liliopsida; Poaceae; PACCAD clade; Andropogoneae; Zea.
REFERENCE	A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.	REFERENCE	1 (bases 1 to 469)
AUTHORS	Unpublished.	AUTHORS	1 (bases 1 to 469)
COMMENT	Contact: Shoemaker R/ Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu	COMMENT	Unpublished.
JOURNAL	This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information	FEATURES Source	Department of Biological Sciences Stanford University, Palo Alto, CA 94304, USA 855 California Ave. Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 1091028 row: H column: 03. Location/Qualifiers
REFERENCE	1..469	/organism="Zea mays"	



Db	253	ATGTCTTAACACCAAAAGCTTCAATTGTTAATTGGGG 2^o4	SOURCE ORGANISM	Pinus taeda (loblolly pine) Pinus taeda
RESULT	6		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
LOCUS	BX253518	528 bp mRNA linear EST 24-FEB-2003	Bukaryota; Viridiplantae; Streptophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.	
DEFINITION	BX253518	Pinus pinaster differentiating xylem adult Pinus pinaster	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	
ACCESSION	BX253518	CDNA clone PP08410 similar to PYROPHOSPHATE ENERGIZED VACUOLAR	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	
VERSION	BX253518	MEMBRANE PROTON PUMP, mRNA sequence.	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	
KEYWORDS	BST.	BX253518.1 GI:28520427	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	
SOURCE	Pinus pinaster	Pinus pinaster	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	
ORGANISM	Pinus pinaster	Pinus pinaster	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	
REFERENCE				
AUTHORS			1 (bases 1 to 576)	
TITLE			Sederoff, R.	
COMMENT			Molecular Basis of Wood Formation in the Pine Megagenome	
CONTACT			Unpublished	
FOREST BIOTECHNOLOGY			Contact: Sederoff, Ron	
North Carolina State University			Forest Biotechnology	
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,			North Carolina State University	
NC 27695, USA			840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,	
TEL:	919 515 7800		NC 27695, USA	
FAX:	919 515 7801		TEL:	
Email:	ron_sederoff@ncsu.edu		FAX:	
Please see <a href="http://web.ahc.umn.edu/biodata/nsfpine/">http://web.ahc.umn.edu/biodata/nsfpine/</a> for further information.			Email:	
Seq primer:	T3		Please see <a href="http://web.ahc.umn.edu/biodata/nsfpine/">http://web.ahc.umn.edu/biodata/nsfpine/</a> for further information.	
FEATURES	source	Location/Qualifiers		
		1..576	/organism="Pinus taeda"	
			/mol_type="mRNA"	
			/strain="Coastal plain loblolly pine from North Carolina"	
			/db_xref="3352"	
			/clone="NRV099_B05"	
			/tissue_type="xylem"	
			/cell_type="Root (primary)"	
			/dev_stages="Transitional"	
			/lab_host="XL1-Blue"	
			/clone_id="NRV"	
			/note="Vector: pBlueScript SK-, Site 1: Eco RI; Site 2: Xba I; Host: XL1-Blue"	
			XhoI: The library is from primary xylem scraped from the roots of a twelve year old tree in the transitional phase from juvenile wood to mature wood production. NOTE: The sequences contain a 'CDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 5'-AAATGGCACGAG-'.	
BASE COUNT	134 a 109 c 142 g 172 t 19 others			
ORIGIN				
Query Match	30.1%	Score 31.6; DB 13; Length 576;		
Best Local Similarity	56.9%	Pred. No. 7.4; Mismatches 44; Indels 0; Gaps 0;		
Matches	58;	Conservative		
DEFINITION				
ACCESSION	AL564798/c			
VERSION	AL564798.2			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
			Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 1201)			
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polaves,D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
COMMENT	On Feb 16, 2001 this sequence version replaced 9i:12915562.			
CONTACT	Genoscope			
Genoscope - Centre National de Sequençage				
RESULT	7			
LOCUS	BQ655776	576 bp mRNA linear EST 07-MAY-2003		
DEFINITION	NRV099_B05_F	(Nsf Xylem Root wood Vertical) Pinus taeda cDNA		
	clone NRV099_B05_5'	similar to Arabidopsis thaliana sequence		
	At1g15690	putative protein see <a href="http://mips.gsf.de/proj/thal/db/index.html">http://mips.gsf.de/proj/thal/db/index.html</a> , mRNA sequence.		
ACCESSION	BQ655776.1	GI:21788102		
VERSION				
KEYWORDS				

BP 191 91006 EVRY cedex - France  
 Email: [segref@genoscope.cnrs.fr](mailto:segref@genoscope.cnrs.fr); Web : [www.genoscope.cnrs.fr](http://www.genoscope.cnrs.fr)  
 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8337.r. For more information about this cluster, see <http://www.genoscope.cnrs.fr/cgi-bin/cluster.cgi?seq=CSODM007DA01QPI&cluster=8337.r>. Contact : Peng Liang Email : [fliang@lifetch.com](mailto:fliang@lifetch.com); Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODM007DA01QPI.  
 FEATURES  
 Source  
 1. .1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3606"  
 /clone="CSODM007B02"  
 /tissue\_type="FETAL LIVER"  
 /dev\_stage="Fetal"  
 /clone\_lib="Homo sapiens FETAL LIVER"  
 /note="Organ: liver; Vector: pCMVSPORT\_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT\_6 vector. Library was not normalized."  
 ASE COUNT 320 a 282 g 272 t 135 others  
 RIGIN Query Match 29.3%; Score 30.8; DB 9; Length 1201;  
 Best Local Similarity 38.7%; Pred. No. 17;  
 Matches 24; Conservative 25; Mismatches 13; Indels 0; Gaps 0;  
 Y 21 TAGGGGTATTGSGTCAGCATCACACCAAAAAAGCTATGCCCTCTTACAACCG 80  
 b 1181 WAMGGGRKCKRKYMAVRWAAACMMAAARAKTCTKTTSKXTTTTNCANSS 1122  
 Y 81 TG 82  
 b 1121 GG 1120

ORIGIN Query Match 29.1%; Score 30.6; DB 13; Length 463;  
 Best Local Similarity 60.0%; Pred. No. 15;  
 Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
 Qy 5 TTAGTTCTCTCGCTTACTGGGTTATIGTCAGCATCACACCAAAAAGTCATGC 64  
 Db 457 TTCCCTGATACTATGTAAGGGTATTAGGGTATCAGGATCATAGCAGACCGAATTATCTT 398  
 Qy 65 GCCTCTTACAACTGTATTC 89  
 Db 397 GTCATCTTCTCACCCTGTAATC 373

RESULT 10  
 CA31548/c  
 LOCUS CR341548  
 DEFINITION *Ek14a02.x1* zebrafish fin day3 regeneration *Danio rerio* cDNA 3', mRNA sequence.  
 ACCESSION CA341548  
 VERSION GI:24559644  
 KEYWORDS EST.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 (bases 1 to 472)

REFERENCE 1  
 AUTHORS Clark, M.; Johnson, S. L.; Lehrach, H.; Lee, R.; Li, F.; Marrs, M.; Eddy, S.; Hillier, L.; Kucaba, T.; Martin, J.; Beck, C.; Wyllie, T.; Underwood, K.; Stepcoski, M.; Theising, B.; Allen, M.; Bowers, Y.; Person, B.; Swaller, T.; Gibbons, M.; Pape, D.; Harvey, N.; Schurk, R.; Ritter, E.; Kohn, S.; Shin, T.; Jackson, Y.; Cardenas, M.; McCann, R.; Waterston, R.; and Wilson, R.

TITLE WashU Zebrafish EST Project 1998  
 JOURNAL Unpublished  
 COMMENT Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: [zebrafish@watson.wustl.edu](mailto:zebrafish@watson.wustl.edu)  
 DNA Library Preparation: Raymond Lee, cDNA Library Arrayed by: Matthew Clark, DNA Sequencing by: Washington University Genome Sequencing Center, Clone distribution: Genome Systems, St. Louis, Missouri (web address: [www.genomesystems.com](http://www.genomesystems.com)) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: [www.resgen.com](http://www.resgen.com)) (email contact: info@resgen.com) and RessourcenZentrumPrimerDatenbank, Berlin, Germany (web address: [www.rzpd.de](http://www.rzpd.de)) Seq Primer: T7 from Gibco  
 High quality sequence stop: 394.  
 Location/Qualifiers 1..472  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /sex="mixed male and female"  
 /tissue\_type="3 day fin regeneration"  
 /lab\_host="B. coli XLOR"  
 /clones\_1lib="zebrafish fin day3 regeneration"  
 /note="Vector: PBK-CMV; Site: 1; ECORI; Site: 2; XbaI; 1st strand cDNA primed with (GA)TOACTGTCAG[AT]18, followed by second strand synthesis, and ligated to 5' adapter (5'-attccggcgcagg-3', 3'-gcgggtatctc-5'). cDNA was cloned directionally (ECORI/XbaI) into Stratagene Zap express lambda phage arms. Mass in vivo excision done to obtain insert in PBK-CMV phagemid."  
 BASE COUNT 202 a 80 c 78 g 112 t  
 ORIGIN Query Match

Best Local Similarity	63.9%	Pred. No.	18/	
Matches	46;	Conservative	0;	Mismatches
Qy	1 CCGTTTACTTCTCGCTTAGGGTTATGGCAGCATCACACAAAAACTCA	60	0;	Indels
Ds	73 CTCCTTATTGTTGTTTCATTTTGTACAACTGCTAAT	14	0;	Gaps
Qy	61 TGGTGCCCTCTT	72		
Ds	13 TGATGCCATT	2		
RESULT	11			
LOCUS	BP166498	873 bp	mRNA	linear EST 30-OCT-2000
DEFINITION	601774993FL NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3955615			
KEYWORDS	mRNA sequence.			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 873)			
REFERENCE	BP166498			
AUTHORS	BP166498.1 GI:11046850			
VERSION				
SOURCE	Mus musculus (house mouse)			
COMMENT	Unpublished			
FEATURES	Source			
COMMENT	Tissue Procurement: Gilbert Smith, Ph.D.			
COMMENT	CDNA Library Preparation: Life Technologies, Inc.			
COMMENT	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LJNL)			
COMMENT	DNA Sequencing by: Incyte Genomics, Inc. Consortium			
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LJNL at: http://image.ljnl.gov			
Plate:	LJLM9215 row: 1 column: 24			
Plates:	LJLM9215 row: 1 column: 24			
High quality sequence stop:	641.			
Location/Qualifiers	1. 873			
COMMENT	/organism="Mus musculus"			
COMMENT	/mol_type="mRNA"			
COMMENT	/strain="CZECII"			
COMMENT	/db_xref="Taxon:10090"			
COMMENT	/clone="IMAGE:395615"			
COMMENT	/tissue_type="spontaneous tumor, metastatic to mammary, stem cell, origin."			
COMMENT	/lab_host="DH10B"			
COMMENT	/clone_id="NCI CGAP Lu29"			
COMMENT	/note="Organ: lung; Vector: PCMV-SPORT6, Site:1: SalI; Site:2: Nci; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"			
BASE COUNT	221 a 195 c 237 g 220 t			
ORIGIN				
RESULT	13			
LOCUS	BI805751/c	664 bp	mRNA	linear EST 02-OCT-2001
DEFINITION	S041C04 stem library from Oryza sativa (3-5 leaf stage) Oryza			
ORGANISM	Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.			
REFERENCE	(bases 1 to 664)			
AUTHORS	Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.			
TITLE	A Gene Expression Screen in Oryza sativa			
JOURNAL	Unpublished			
COMMENT	Contact: Dong HT			
COMMENT	Laboratory of Functional Genetics			
COMMENT	Bio-technology Institute of Zhejiang University			
COMMENT	Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China			
COMMENT	Tel: 0086-571-86872051			
COMMENT	Fax: 0086-571-86961525			
COMMENT	Email: hdong@zju.edu.cn			
FEATURES	Location/Qualifiers			
SEQ PRIMER	Unpublished			
LOCUS	BUB73870	617 bp	mRNA	linear EST 16-OCT-2002

source	1. .664 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:4530" /clone="IS047C04" /tissue_type="Stem" /dev_stage="3-5 leaf stage" /clone_lib="Stem library from Oryza sativa (3-5 leaf stage)" /note="vector: pSport2" base count 192 a 167 c 138 g 167 t origin	Db	155 TGTCACTTCTCACCCGTGATCAAATC 130  RESULT 15 CB214094/C LOCUS CB214094 Oryza minuta HybrizAP-2.1 XR library Oryza minuta cDNA 5', mRNA linear EST 05-FEBB-2003 DEFINITION OML04374 Oryza minuta HybrizAP-2.1 XR library Oryza minuta cDNA 5', mRNA sequence. ACCESSION CB214094 VERSION CB214094.1 GI:28260185 KEYWORDS EST. SOURCE Oryza minuta ORGANISM Oryza minuta Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; Ehrhartoidae; Oryzeae; Oryzae. 1 (bases 1 to 671) REFERENCE AUTHORS J.S. TITLE HybrizAP-2.1 XR library JOURNAL unpublished COMMENT Contact: Jeong Sheop Shin Plant Molecular Genetics Graduate School of Biotechnology, University of Korea 136-701 Anam-dong 51, Seoul, Korea Tel: 00 82 2 3390 3430 Fax: 00 82 2 927 9028 Email: jsshin@kuccnx.korea.ac.kr. Location/Qualifiers 1. .671 /organism="Oryza minuta" /mol_type="mRNA" /db_xref="taxon:63629" /dev_stage="4 weeks after Germination" /clone_lib="Oryza minuta HybrizAP-2.1 XR library" /note="Organ: immature leaf" base count 181 a 152 c 160 g 178 t origin
source	2. .664 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:4530" /clone="IS047C04" /tissue_type="Stem" /dev_stage="3-5 leaf stage" /clone_lib="Stem library from Oryza sativa (3-5 leaf stage)" /note="vector: pSport2" base count 192 a 167 c 138 g 167 t origin	Db	156 TGTCACTTCTCACCCGTGATCAAATC 130  RESULT 16 AU091984/C LOCUS AU091984 Rice root Oryza sativa (japonica cultivar-group) cDNA clone R0240, mRNA sequence. AU091984 UNPUBLISHED AU091984.1 GI:8404630 EST. REFERENCE AUTHORS Sasaki, T. and Yamamoto, K. TITLE Rice cDNA from root (2000) JOURNAL Unpublished COMMENT Contact: Takuji Sasaki National Institute Of Agrobiological Resources, Kannondai 2-1-2, Tsukuba, Ibaraki Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki Tel: 81-298-38-1441 Fax: 81-298-38-7468 Email: tssasaki@abraffrc.90.jp, URL: <a href="http://rbp.dna.affrc.go.jp/">http://rbp.dna.affrc.go.jp/</a> PROJECT "-RGP", PROJID "RGP", LOCATION/QUALIFIERS 1. .671 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /clone="R0240" /clone_lib="Rice root" /note="Prepared from seedling root." base count 196 a 169 c 136 g 168 t 2 others origin
source	3. .664 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:4530" /clone="IS047C04" /tissue_type="Stem" /dev_stage="3-5 leaf stage" /clone_lib="Stem library from Oryza sativa (3-5 leaf stage)" /note="vector: pSport2" base count 192 a 167 c 138 g 167 t origin	Db	157 TGTCACTTCTCACCCGTGATCAAATC 130  RESULT 17 AU091984/C LOCUS AU091984 Rice root Oryza sativa (japonica cultivar-group) cDNA clone R0240, mRNA sequence. AU091984 UNPUBLISHED AU091984.1 GI:8404630 EST. REFERENCE AUTHORS Sasaki, T. and Yamamoto, K. TITLE Rice cDNA from root (2000) JOURNAL Unpublished COMMENT Contact: Takuji Sasaki National Institute Of Agrobiological Resources, Kannondai 2-1-2, Tsukuba, Ibaraki Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki Tel: 81-298-38-1441 Fax: 81-298-38-7468 Email: tssasaki@abrraffrc.90.jp, URL: <a href="http://rbp.dna.affrc.go.jp/">http://rbp.dna.affrc.go.jp/</a> PROJECT "-RGP", PROJID "RGP", LOCATION/QUALIFIERS 1. .671 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /clone="R0240" /clone_lib="Rice root" /note="Prepared from seedling root." base count 196 a 169 c 136 g 168 t 2 others origin
source	4. .664 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:4530" /clone="IS047C04" /tissue_type="Stem" /dev_stage="3-5 leaf stage" /clone_lib="Stem library from Oryza sativa (3-5 leaf stage)" /note="vector: pSport2" base count 192 a 167 c 138 g 167 t origin	Db	158 TGTCACTTCTCACCCGTGATCAAATC 130  RESULT 18 AU091984/C LOCUS AU091984 Rice root Oryza sativa (japonica cultivar-group) cDNA clone R0240, mRNA sequence. AU091984 UNPUBLISHED AU091984.1 GI:8404630 EST. REFERENCE AUTHORS Sasaki, T. and Yamamoto, K. TITLE Rice cDNA from root (2000) JOURNAL Unpublished COMMENT Contact: Takuji Sasaki National Institute Of Agrobiological Resources, Kannondai 2-1-2, Tsukuba, Ibaraki Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki Tel: 81-298-38-1441 Fax: 81-298-38-7468 Email: tssasaki@abrraffrc.90.jp, URL: <a href="http://rbp.dna.affrc.go.jp/">http://rbp.dna.affrc.go.jp/</a> PROJECT "-RGP", PROJID "RGP", LOCATION/QUALIFIERS 1. .671 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /clone="R0240" /clone_lib="Rice root" /note="Prepared from seedling root." base count 196 a 169 c 136 g 168 t 2 others origin